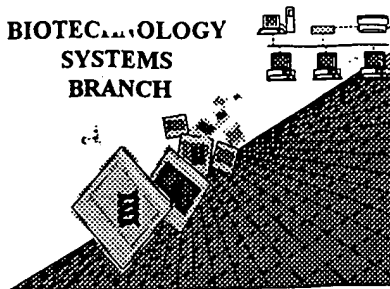


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/765,614A

Source: 1619

Date Processed by STIC: 6/20/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

RECEIVED

## Raw Sequence Listing Error Summary

JUL 11 2001

TECH CENTER 1600/2900  
09/26/99

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>09/26/99</u>
ATTN NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> <u>Wrapped Nucleics</u> <u>Wrapped Aminos</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

RECEIVED<sup>9</sup>

JUL 11 2001

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001  
TIME: 11:00:39

TECH CENTER 1600/2900

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

Does Not Comply  
Corrected Diskette Needed

pg 1-6

6 <110> APPLICANT: Nycomed Imaging AS  
 8 <120> TITLE OF INVENTION: Improvements in or relating to  
 9 diagnostic/therapeutic  
 10 agents  
 12 <130> FILE REFERENCE: REF/Klaveness/054C  
 14 <140> CURRENT APPLICATION NUMBER: US/09/765,614A  
 15 <141> CURRENT FILING DATE: 2001-01-22  
 17 <160> NUMBER OF SEQ ID NOS: 25 31 (p. 6)  
 19 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

36 <210> SEQ ID NO: 2  
 37 <211> LENGTH: 25  
 38 <212> TYPE: PRT  
 39 <213> ORGANISM: Artificial Sequence  
 41 <220> FEATURE:  
 42 <223> OTHER INFORMATION: Description of Artificial  
 43 Sequence: Peptide  
 44 comprising  
 45 phosphatidylserine-binding and  
 46 heparin-binding sections  
 48 <400> SEQUENCE: 2  
 49 Phe Asn Phe Arg Leu Lys Ala Gly Gln  
 50 Lys Ile Arg Phe Gly Ala Ala  
 51 1 5  
 52 10 15  
 54 Ala Trp Glu Pro Pro Arg Ala Arg Ile  
 56 20 25  
 127 <210> SEQ ID NO: 7  
 128 <211> LENGTH: 13  
 129 <212> TYPE: PRT  
 130 <213> ORGANISM: Artificial Sequence  
 132 <220> FEATURE:  
 133 <223> OTHER INFORMATION: Description of Artificial  
 134 Sequence: Lipopeptide  
 135 consisting of a heparin  
 136 sulphate binding peptide  
 137 and a fibronectin peptide  
 139 <220> FEATURE:  
 140 <221> NAME/KEY: MOD\_RES  
 141 <222> LOCATION: (1)  
 142 <223> OTHER INFORMATION: Dipalmitoyl-lysine  
 144 <400> SEQUENCE: 7  
 145 Lys Lys Arg Lys Arg Trp Gln Pro Pro  
 146 Arg Ala Arg Ile

mod up  
 Mod lines up - Per 1.823  
 of Sequence Rules,  
 a MAXIMUM of  
 4 lines for <223>  
 response

same error

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

RECEIVED

JUL 11 2001

TECH CENTER 1600/2900

E--> 147 1 5  
E--> 148 10  
151 <210> SEQ ID NO: 8  
152 <211> LENGTH: 24  
153 <212> TYPE: PRT  
154 <213> ORGANISM: Artificial Sequence  
156 <220> FEATURE:  
157 <223> OTHER INFORMATION: Description of Artificial  
158 Sequence:Fibronectin  
159 peptide sequence  
161 <400> SEQUENCE: 8  
162 Phe Asn Phe Arg Leu Lys Ala Gly Gln  
E--> 163 Lys Ile Arg Phe Gly Gly Gly  
164 1 5  
E--> 165 10 15  
167 Gly Trp Gln Pro Pro Arg Ala Ile  
E--> 169 20  
193 <210> SEQ ID NO: 10  
194 <211> LENGTH: 10  
195 <212> TYPE: PRT  
196 <213> ORGANISM: Artificial Sequence  
198 <220> FEATURE:  
199 <223> OTHER INFORMATION: Description of Artificial  
200 Sequence:Biotinylated  
201 fibrin-anti-polymerant peptide  
203 <220> FEATURE:  
204 <221> NAME/KEY: MOD\_RES  
205 <222> LOCATION: (1)  
206 <223> OTHER INFORMATION: Biotinylated-Gly  
208 <220> FEATURE:  
209 <221> NAME/KEY: MOD\_RES  
210 <222> LOCATION: (10)  
211 <223> OTHER INFORMATION: AMIDATION  
213 <400> SEQUENCE: 10  
214 Gly Pro Arg Pro Pro Glu Arg His Gln  
E--> 215 Ser  
E--> 216 1 5  
E--> 217 10  
249 <210> SEQ ID NO: 12  
250 <211> LENGTH: 18  
251 <212> TYPE: PRT  
252 <213> ORGANISM: Artificial Sequence  
254 <220> FEATURE:  
255 <223> OTHER INFORMATION: Description of Artificial  
256 Sequence:Endothelial  
257 cell binding lipopeptide  
259 <220> FEATURE:  
260 <221> NAME/KEY: MOD\_RES  
261 <222> LOCATION: (1)

## RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

262 <223> OTHER INFORMATION: 2-n-hexadecylstearyl-Lys  
 264 <220> FEATURE:  
 265 <221> NAME/KEY: MOD\_RES  
 266 <222> LOCATION: (18)  
 267 <223> OTHER INFORMATION: AMIDATION  
 269 <400> SEQUENCE: 12  
 270 Lys Leu Ala Leu Lys Leu Ala Leu Lys  
 E--> 271 Ala Leu Lys Ala Ala Leu Lys  
 272 1 5  
 E--> 273 10 15  
 275 Leu Ala  
 312 <210> SEQ ID NO: 14  
 313 <211> LENGTH: 13  
 314 <212> TYPE: PRT  
 315 <213> ORGANISM: Artificial Sequence  
 317 <220> FEATURE:  
 318 <223> OTHER INFORMATION: Description of Artificial  
 319 Sequence:Lipopeptide  
 320 with an affinity for  
 321 endothelial cells  
 323 <220> FEATURE:  
 324 <221> NAME/KEY: MOD\_RES  
 325 <222> LOCATION: (1)  
 326 <223> OTHER INFORMATION: Dipalmitoyl-Lys  
 328 <220> FEATURE:  
 329 <221> NAME/KEY: MOD\_RES  
 330 <222> LOCATION: (4)  
 331 <223> OTHER INFORMATION: Acp  
 333 <220> FEATURE:  
 334 <221> NAME/KEY: MOD\_RES  
 335 <222> LOCATION: (13)  
 336 <223> OTHER INFORMATION: AMIDATION  
 338 <400> SEQUENCE: 14  
 W--> 339 Lys Lys Lys Xaa Ile Arg Arg Val Ala  
 E--> 340 Arg Pro Pro Leu  
 E--> 341 1 5  
 E--> 342 10  
 345 <210> SEQ ID NO: 15  
 346 <211> LENGTH: 14  
 347 <212> TYPE: PRT  
 348 <213> ORGANISM: Artificial Sequence  
 350 <220> FEATURE:  
 351 <223> OTHER INFORMATION: Description of Artificial  
 352 Sequence:Lipopeptide  
 353 comprising an interleukin-1  
 354 receptor binding  
 W--> 355 peptide  
 357 <220> FEATURE:  
 358 <221> NAME/KEY: MOD\_RES

RECEIVED

JUL 11 2001

TECH CENTER 1600/2900

## RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

359 <222> LOCATION: (1)  
 360 <223> OTHER INFORMATION: Dipalmitoyl-Lys  
 362 <400> SEQUENCE: 15  
 363 Lys Gly Asp Trp Asp Gln Phe Gly Leu  
 E--> 364 Trp Arg Gly Ala Ala *same*  
 365 1 5  
 E--> 366 10  
 369 <210> SEQ ID NO: 16  
 370 <211> LENGTH: 12  
 371 <212> TYPE: PRT  
 372 <213> ORGANISM: Artificial Sequence  
 374 <220> FEATURE:  
 375 <221> NAME/KEY: MOD\_RES  
 376 <222> LOCATION: (1)  
 377 <223> OTHER INFORMATION: Dabsyl-Tyr  
 379 <220> FEATURE:  
 380 <221> NAME/KEY: MOD\_RES  
 381 <222> LOCATION: (10)  
 382 <223> OTHER INFORMATION: RGDS chain linked via NH2 group  
 383 of lysine  
 385 <220> FEATURE:  
 386 <223> OTHER INFORMATION: Description of Artificial  
 387 Sequence: Branched core  
 388 peptide comprising a dabsylated  
 389 atherosclerotic  
 W--> 390 plaque-binding sequence and  
 W--> 391 RGDS  
 393 <400> SEQUENCE: 16  
 394 Tyr Arg Ala Leu Val Asp Thr Leu Lys  
 E--> 395 Lys Gly Cys *same*  
 E--> 396 1 5  
 E--> 397 10  
 400 <210> SEQ ID NO: 17  
 401 <211> LENGTH: 25  
 402 <212> TYPE: DNA  
 403 <213> ORGANISM: Artificial Sequence  
 405 <220> FEATURE:  
 406 <223> OTHER INFORMATION: Description of Artificial  
 407 Sequence: Synthetic  
 408 oligonucleotide  
 410 <220> FEATURE:  
 411 <221> NAME/KEY: misc\_feature  
 412 <222> LOCATION: (1)  
 413 <223> OTHER INFORMATION: Biotinylated  
 415 <400> SEQUENCE: 17  
 E--> 416 gaaaggtagt ggggtcgtgt gccgg 25  
 417  
 419 <210> SEQ ID NO: 18  
 420 <211> LENGTH: 15

*see item 1 on Eva summary sheet*

## RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

421 <212> TYPE: PRT  
422 <213> ORGANISM: Artificial Sequence  
424 <220> FEATURE:  
425 <223> OTHER INFORMATION: Description of Artificial  
426 Sequence:Lipopeptide  
427 with affinity for thrombi *thrombin?*  
429 <220> FEATURE:  
430 <221> NAME/KEY: MOD\_RES  
431 <222> LOCATION: (1)  
432 <223> OTHER INFORMATION: Dipalmitoyl-Lys  
434 <220> FEATURE:  
435 <221> NAME/KEY: MOD\_RES  
436 <222> LOCATION: (15)  
437 <223> OTHER INFORMATION: AMIDATION  
439 <400> SEQUENCE: 18  
440 Lys Asn Asp Gly Asp Phe Glu Glu Ile  
E--> 441 Pro Glu Glu Tyr Leu Gln *same*  
442 1 5  
E--> 443 10 15  
680 <210> SEQ ID NO: 27  
681 <211> LENGTH: 16  
682 <212> TYPE: PRT  
683 <213> ORGANISM: Artificial Sequence  
685 <220> FEATURE:  
686 <223> OTHER INFORMATION: Description of Artificial  
687 Sequence:Atherosclerotic  
688 plaque-binding peptide  
690 <400> SEQUENCE: 27  
691 Tyr Ala Lys Phe Arg Glu Thr Leu Glu  
E--> 692 Asp Thr Arg Asp Arg Met Tyr *same*  
693 1 5  
E--> 694 10 15  
697 <210> SEQ ID NO: 28  
698 <211> LENGTH: 17  
699 <212> TYPE: PRT  
700 <213> ORGANISM: Artificial Sequence  
702 <220> FEATURE:  
703 <223> OTHER INFORMATION: Description of Artificial  
704 Sequence:Atherosclerotic  
705 plaque-binding peptide  
707 <400> SEQUENCE: 28  
708 Arg Ala Leu Val Asp Thr Glu Phe Lys  
E--> 709 Val Lys Gln Glu Ala Gly Ala *same*  
710 1 5  
E--> 711 10 15  
713 Lys  
718 <210> SEQ ID NO: 29  
719 <211> LENGTH: 14  
720 <212> TYPE: PRT

## RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

721 <213> ORGANISM: Artificial Sequence  
 723 <220> FEATURE:  
 724 <223> OTHER INFORMATION: Description of Artificial  
 725 Sequence:Thrombus  
 726 binding peptide  
 728 <400> SEQUENCE: 29  
 729 Asn Asp Gly Asp Phe Glu Glu Ile Pro  
 E--> 730 Glu Glu Tyr Leu Gln *none*  
 731 1 5  
 E--> 732 10  
 751 <210> SEQ ID NO: 31  
 752 <211> LENGTH: 13  
 753 <212> TYPE: PRT  
 754 <213> ORGANISM: Artificial Sequence  
 756 <220> FEATURE:  
 757 <223> OTHER INFORMATION: Description of Artificial  
 758 Sequence:Platelet  
 759 binding peptide  
 761 <400> SEQUENCE: 31  
 762 Pro Leu Tyr Lys Lys Ile Ile Lys Lys  
 E--> 763 Leu Leu Glu Ser *none*  
 E--> 764 1 5  
 E--> 765 10

*PMI*  
**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



## VERIFICATION SUMMARY

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:40

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number.  
L:46 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:50 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:137 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:146 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
M:332 Repeated in SeqNo=7  
L:163 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
M:332 Repeated in SeqNo=8  
L:215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10  
M:332 Repeated in SeqNo=10  
L:230 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12  
M:332 Repeated in SeqNo=12  
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:340 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14  
M:332 Repeated in SeqNo=14  
L:355 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:364 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15  
M:332 Repeated in SeqNo=15  
L:390 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:391 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:395 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
M:332 Repeated in SeqNo=16  
L:416 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:17  
L:441 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18  
M:332 Repeated in SeqNo=18  
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:692 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27  
M:332 Repeated in SeqNo=27  
L:709 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28  
M:332 Repeated in SeqNo=28  
L:730 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29  
M:332 Repeated in SeqNo=29  
L:763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31  
M:332 Repeated in SeqNo=31  
L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (25) Counted (31)